

FIG. 1

ATGACGTCCACCTGCACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCC
CTCTCCAAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGGTTATC
TTCCTCGCCCGCTCTTTCGTGCGCAACATAGTGTGGCGCTAGTGTTGAGCGCAAGCCG
CAGCTGCTGCAGGTGACCAACCGTTTATCTTTAACCTCCTCGTCACCGACCTGCTGCAG
ATTTCGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTCTTCTGGCCCCCTCAAC
AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTGCCTTTCGCCAGCGCTCAAC
ACCATTGTCTTGGTGTCACTGGATCGCTACTTGTCCATCATCCACCCTCTCTCTACCCG
TCCAAGATGACCCAGCGCGCGGTTACCTGCTCCTCTATGGCACCCTGGATTGTGGCCATC
CTGCAGAGCACTCCTCCTACTACGGCTGGGGCCAGGCTGCCCTTGTATGAGCGCAATGCT
CTCTGCTCCATGATCTGGGGGGCCAGCCCAGCTACACTATTCTCAGCGTGGTGTCTCTC
ATCGTCATTCCACTGATTGTCTATGATTGCCTGCTACTCCGTGGTGTCTGTGACGCCCG
AGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAAGTGCAGTCAAGGAC
TGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTTCCAGGATGAGAGT
GAGTTTCGCCCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAAATGGAAGCCAAAG
GACGGCAGCTGAAGGCCAAGGAAGGAACACGGGGACAGTGAGAGTAGTGTAGAGGCC
AGGGGCAGCGAGGAGGTCAAGAGAGCAGCAGCGTGGCCAGCAGCGCAGCATGGAGGGT
AAGGAAGGCAGCACCAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTGCACAGAG
GTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTTGGTGAAGACGACATC
AATTTTCAGTGAGGATGACGCTGAGGCAGTGAACATCCCCGAGAGCCTCCCACCCAGTCGT
CGTAACAGCAACAGCAACCCCTCCTCTGCCAGGTGCTACCAAGTGCAAAAGCTGCTAAAGTG
ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTCAGCATC
CTGGCCGTGTGGGTGGATGTGAAACCCAGGTACCCAGTGGGTGATCACCATAATCATC
TGGCTTTTCTTCTGCACTGCTGCATCCACCCCTATGCTATGCTATGCTACATGCACAAGACC
ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAGCCCCGAAA
GAAGATAGCCACCCAGACCTGCCCGAACAGAGGGTGGGACTGAAGSCAAGATTGTCCTC
TCCTACGATTCTGCTACTTTTTCCTTGA

FIG. 3

GCAACCTGTCTCACGCCCTCTGGCTGTTGCC

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FIG. 4

AGTTAGTTCTAAGGCAAACCTT

FIG. 5

1 MTSTCTNSTR ESNSSHTCMP LSKMPISLAH GIIRSTVLVI FLAASFVGNI
51 VLALVLQRKP QLLQVTNRFI FNLVTDLLQ ISLVAPWVVA TSVPLFWPLN
101 SHFCTALVSL THLFAFASVN TIVLVSVDRY LSIHPLSYF SKMTQRRGYL
151 LLYGTWIVAI LQSTPPLYGW GQAAFDERNA LCSMIWGASP SYTILSVVSF
201 IIVIPLIVMIA CYSVVFCAR RQHALLYNVK RLSLEVRVKD CVENEDEEGA
251 EKKEEFQDES EFRQHEGEV KAKEGRMEAK DGSLLAKEGS TGTSESSVEA
301 RGSEEVRESS TVASDGSMEG KEGSTKVEEN SMKADKGRTE VNQCSIDLGE
351 DDMEFGEDDI NFEDDVEAV NIPESLPSPR RNSNSNPPLP RCYQCKAAKV
401 IFIIIFSIVL SLGPYCFLAV LAVWVDVETQ VPQWVITIII WLFFLQCCIH
451 PYVYGYMHKT IKKEIQDMLK KFFCKEKKPPK EDSHPDLPQT EGGTEGKIVP
501 SYDSATFP

FIG. 6A

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ACM4_CHICK      ~~~~~~MANFTFGDLALDVARMGGIALSTPSGRLSTGLTTPGLSPT
YDBM_CAEEL     ~~~~~~MTFRDLLSVSFEGPRPDSSAGGSSAGGGGGSGAGGAAPSEG
5H1A_HUMAN      ~~~~~~MTFRDILSVTFEGRPRSSSTGGSGAGGGAGVTG...P.EG
5H1A_MOUSE      ~~~~~~Q13675
5HT_LYST        ~~~~~~Q13729
O60451          ~~~~~~O60451
A1AA_RAT        ~~~~~~A1AA_RAT
O54913          ~~~~~~O54913
A1AA_BOVIN      ~~~~~~A1AA_BOVIN
A1AA_CANFA      ~~~~~~A1AA_CANFA
A1AA_RABIT      ~~~~~~A1AA_RABIT
A1AA_HUMAN      ~~~~~~A1AA_HUMAN
A1AA_ORYLA      ~~~~~~A1AA_ORYLA
O96716          ~~~~~~O96716
O75963          ~~~~~~O75963
HGPRBMY8       ~~~~~~HGPRBMY8

ACM4_CHICK      ~~~~~~MCFAEKGEAGEDVDVHHSLFC.P.KKLVGNL...KGFFIR
YDBM_CAEEL     ~~~~~~MDV..LSPGQ...GNNTT...SPPAPETGNG
5H1A_HUMAN      ~~~~~~MDV..LSPGQ...GNNTT...SPPAPETGNG
5H1A_MOUSE      ~~~~~~MDM...FSLGQ...GNNTT...TSLEPGFTGGN
5H1A_FUGRU      ~~~~~~MDLRATSSND...SNATSGYSDTAAWDWDEGN
5HT_LYST        ~~~~~~GLVTSDFDNISYGLT.GQFNIGSHSRSDRNASANDTSATN
A1AD_HUMAN      ~~~~~~PAVGVPVPGAGGGGGVVGAGSGEDNRSSAGEPGSAGGGG
A1AD_MOUSE      ~~~~~~PAVGGV.P.GATGGSAVVGTGSGEDNQSSSTAFAAGA...SSE
Q13675         ~~~~~~MMFLSCNASHS
Q13729         ~~~~~~MMFLSCNASHS
O60451         ~~~~~~MMFLSCNASHS
A1AA_RAT        ~~~~~~MMFLSCNASHS
O54913         ~~~~~~MMFLSCNASHS
A1AA_BOVIN      ~~~~~~MMFLSCNASHS
A1AA_CANFA      ~~~~~~MMFLSCNASHS
A1AA_RABIT      ~~~~~~MMFLSCNASHS
A1AA_HUMAN      ~~~~~~MMFLSCNASHS
A1AA_ORYLA      ~~~~~~MMFLSCNASHS
O96716         ~~~~~~MPSSVTLNLNC
O75963         ~~~~~~MSANTTVSPTEATTANLANSDEA
HGPRBMY8       ~~~~~~MSLNLSLS
HGPRBMY8       ~~~~~~MTSTCTNSPRENN
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[illegible]

FIG. 6C

ACM4_CHICK IKGYWPLGAVCDLWLAADYVVSNASVMNLLISFDRYFC
YDBM_CAEL IAGEWVEPEDALCEVEVSADILCSTASTWNNISVCEFDRYWA
5H1A_HUMAN VLNKWTILGOVTCDEHIALDVLCTSSILHLCAIALDRYWA
5H1A_MOUSE VLNKWTILGOVTCDEHIALDVLCTSSILHLCAIALDRYWA
5H1A_FUGRU VLNKWTILGODICDEHIALDVLCTSSILHLCAIALDRYWA
5HT_LYMST ISKVWFLHSEVCDMWISVDVLCTASIHHLVALAMDRYWA
A1AD_HUMAN VLGEWAFGRAFCDWAAVDVLCTASIHSLCTTISVDRYVG
A1AD_MOUSE VLGEWPFGRITFCDWAAVDVLCTASIHSLCTTISVDRYVG
Q13675 VLGYWAFGRVFCNWAAVDVLCTASIMGLCTTISIDRYTG
Q13729 VLGYWAFGRVFCNWAAVDVLCTASIMGLCTTISIDRYTG
O60451 VLGYWAFGRVFCNWAAVDVLCTASIMGLCTTISIDRYTG
A1AA_RAT ILGYWAFGRVFCNWAAVDVLCTASIMGLCTTISIDRYTG
O54913 ILGYWAFGRVFCNWAAVDVLCTASIMGLCTTISIDRYTG
A1AA_BOVIN ILGYWAFGRVFCNWAAVDVLCTASIMGLCTTISIDRYTG
A1AA_CANFA ILGYWAFGRVFCNWAAVDVLCTASIMGLCTTISIDRYTG
A1AA_RABIT ILGYWAFGRVFCNWAAVDVLCTASIMGLCTTISIDRYTG
A1AA_HUMAN VLGYWAFGRVFCNWAAVDVLCTASIMGLCTTISIDRYTG
A1AA_ORYLA ILDRWAFGRVFCNWAAVDVLCTASIMSLQISVDRYTG
O96716 ILGYWPFEGG.MCLWVVSDDVNSTASIMNLVYAFDRLA
O75963 IRREWIFGVVNCNFSLLYYLISASMTLGLAIDRYYL
HGPRBMY8 VPLEWPLNSHECTALVSTHLEAFASVNTVIVSVDRYLS

ACM4_CHICK VIKPITYPARRTTKMAGIMTAAMLLSFTLWAPAT.LFW.
YDBM_CAEL ITSPVLYMSKRNRKTAGMTISVWSSAALISLAPL.LGWK
5H1A_HUMAN ITDPIIDVYNKRTPRRAALISLTWELGFTISIPPM.LGW.
5H1A_MOUSE ITDPIIDVYNKRTPRRAALISLTWELGFTISIPPM.LGW.
5H1A_FUGRU ITDPIIDVYNKRTPRRAALLISVTWELGFSISIPPM.LGW.
5HT_LYMST VHS.LDYIRRRSARRIELMTIMVWVEALFISIPPL.FGW.
A1AD_HUMAN VRHSLKYPAINTERKAAAILALLWVALVVSIGPL.LGW.
A1AD_MOUSE VRHSLKYPAINTERKAAAILALLWVALVVSIGPL.LGW.
Q13675 VSYPLRYPTIWTORRGMLALCVWALSISVISIGPL.FGW.
Q13729 VSYPLRYPTIWTORRGMLALCVWALSISVISIGPL.FGW.
O60451 VSYPLRYPTIWTORRGMLALCVWALSISVISIGPL.FGW.
A1AA_RAT VSYPLRYPTIWTORRGVRLALCVWALSISVISIGPL.FGW.
O54913 VSYPLRYPTIWTORRGVRLALCVWALSISVISIGPL.FGW.
A1AA_BOVIN VSYPLRYPTIWTORRGMLALCVWALSISVISIGPL.FGW.
A1AA_CANFA VSYPLRYPTIWTORRGMLALCVWALSISVISIGPL.FGW.
A1AA_RABIT VSYPLRYPTIWTORRGMLALCVWALSISVISIGPL.FGW.
A1AA_HUMAN VSYPLRYPTIWTORRGMLALCVWALSISVISIGPL.FGW.
A1AA_ORYLA VSYPLRYPTIWKRRALLAVMLLWVLSISVISIGPL.FGW.
O96716 ILAPFTYHRTKPTAGILLATVGLISLWLSFTLHQNGWY
O75963 VLYPYVYPMKITGNRAVMALNYIMHSLRGCEPPL.FGWS
HGPRBMY8 ITHPLSYPSKMITORRGYLLLYGTWELVATIQSTPPL.LGW

FIG. 6D

ACM4_CHICK QFIVEKRTVHE....RECYIQFLSNFAVTFGLTAAFYF
 YDBM_CAEEL QTAQTFNLIYEKNNTVROQ..TFLDLEPSYTVSATGSPFI
 5H1A_HUMAN R.TP.EDRSDPDA....CTIS..KDHGYTITSTFGAFYF
 5H1A_MOUSE R.AE.EDRSNPNE....CTIS..KDHGYTITSTFGAFYF
 5H1A_FUGRU R.SA.EDRANPDA....CIIS..QKGYTITSTFGAFYF
 5HT_LYMST R.DPNNPDKTGT....CIIS..QKGYTITSTFGAFYF
 A1AD_HUMAN K.EPVVP.....DERFCGIT..EEPGYVLFSSVCSFYF
 A1AD_MOUSE K.EPVVP.....DERFCGIT..EEPGYVLFSSVCSFYF
 Q13675 R.QPAPE.....DETCCQIN..EEPGYVLFSAIGSFYF
 Q13729 R.QPAPE.....DETCCQIN..EEPGYVLFSAIGSFYF
 O60451 R.QPAPE.....DETCCQIN..EEPGYVLFSAIGSFYF
 A1AA_RAT R.QPAPE.....DETCCQIN..EEPGYVLFSAIGSFYF
 O54913 R.QPAPE.....DETCCQIN..EEPGYVLFSAIGSFYF
 A1AA_BOVIN R.QPAPE.....DETCCQIN..EEPGYVLFSAIGSFYF
 A1AA_CANFA R.QPAPE.....DETCCQIN..EEPGYVLFSAIGSFYF
 A1AA_RABIT R.QPAPE.....DETCCQIN..EEPGYVLFSAIGSFYF
 A1AA_HUMAN R.QPAPE.....DETCCQIN..EEPGYVLFSAIGSFYF
 A1AA_ORYLA K.EPAPE.....DETCKIT..EEPGYVLFSAIGSFYF
 O96716 R.DNQSEALAIYSDPCICIT..ASTGYTIVSSLIIFYF
 O75963 S.VEFDFKWM....CYAAWH..EEPGYVLFQWTCALF
 HGPRBM8 QA.....AFDERNAICSNIWGASPSYITLISVVSIVF

ACM4_CHICK PMVINTVYVHTSLA.SRSRVRRHKPESRKERKCKSSSF
 YDBM_CAEEL PTLIMFVYFQYQAFAKHRQIYRQKVIRKHISTILH
 5H1A_HUMAN PTLILNLVYGRLEKA....RFRIRKTVKKVEK.....
 5H1A_MOUSE PTLILNLVYGRLEKA....RFRIRKTVKKVEK.....
 5H1A_FUGRU PTLILNLVYGRLEKA....RFRIRKTVKKVEK.....
 5HT_LYMST PMILMMYVYIRIHLV....RSRIRKDKFQMTKARL..
 A1AD_HUMAN PMILVILVMYCRVYVV....A.....RSTTRSL..
 A1AD_MOUSE PMILVILVMYCRVYVV....A.....RSTTRSL..
 Q13675 PLAILILVMYCRVYVV....A.....KRESRGL..
 Q13729 PLAILILVMYCRVYVV....A.....KRESRGL..
 O60451 PLAILILVMYCRVYVV....A.....KRESRGL..
 A1AA_RAT PLAILILVMYCRVYVV....A.....KRESRGL..
 O54913 PLAILILVMYCRVYVV....A.....KRESRGL..
 A1AA_BOVIN PLAILILVMYCRVYVV....A.....KRESRGL..
 A1AA_CANFA PLAILILVMYCRVYVV....A.....KRESRGL..
 A1AA_RABIT PLAILILVMYCRVYVV....A.....KRESRGL..
 A1AA_HUMAN PLAILILVMYCRVYVV....A.....KRESRGL..
 A1AA_ORYLA PLAILILVMYCRVYVV....A.....KRESRGL..
 O96716 PLILNLVYFGIIEKA....A.....EQDARKT..
 O75963 PFLVNLVYCYGETIRV....ARV.....KARKY..
 HGPRBM8 PLILVILVACYSVVSCAARRQHA.LLYNVKRHSLVRVRKDCV

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FIG. 6E

ACM4_CHICK	KAPPVKQNNNN	PKRAVEVKKEVRNGKVDQPSAQ	ATG
YDBM_CAEL	EISHVLPTSDEFAKEEEEEEDSESSGQVENGLNGND	AI	.
5H1A_HUMANTGADTRHGASPAPOPK..KSVNG....E..		
5H1A_MOUSEKAGTSFGTSSAPPPK..KSLNG....Q..		
5H1A_FUGRUKASDMCLTLSPAVFHK..RA.NG....D..		
5HT_LYMSTKTEETTLVASPKTEYSVSVDCN	GCNSPD..	
A1AD_HUMANEA.....GKKRE		
A1AD_MOUSEEA.....GKKRE		
Q13675KS.....GKKRK		
Q13729KS.....GKKRK		
O60451KS.....GKKRK		
A1AA_RATKS.....GKKRK		
O54913KS.....GKKRK		
A1AA_BOVINKS.....GKKRK		
A1AA_CANFAKS.....GKKRK		
A1AA_RABITKS.....GKKRK		
A1AA_HUMANKS.....GKKRK		
A1AA_ORYLAKE.....GKIEK		
O96716NA.....LEG...		
O75963HCGTVVIVEEDAQRTGRKNSSTSTSSG..		
HGPRBMY8	ENEDEEGAEEK	EEFQDESEFRQHEGEVKAKE	ERMEANDG
ACM4_CHICK	QQEEK	TSNESSTVSMTQTTKDKPTEILPAGQGQSPAHP	
YDBM_CAEL	.IEED	CEDEDSDEKRDDHTS...MTTVTATVTGPT	EAP
5H1A_HUMAN	..SGSRNWRLGVESKAGGALCANGAVRQGD	DGAAL	EVIE
5H1A_MOUSE	..PGSGDCRRSAENRAVGTPCANGAVRQGED	DATL	EVIE
5H1A_FUGRU	..AVSAEWKRGYKFKP.SSPCANGAVRHGEEMESL	EVIE	
5HT_LYMST	..ST	EKKRRAPFKSYG..CSPRPERKKNRAKLPENAN	
A1AD_HUMAN	..GKAS.....	EVVL	
A1AD_MOUSE	..GKAS.....	EVVL	
Q13675	..SDSE.....	QVTL	
Q13729	..SDSE.....	QVTL	
O60451	..SDSE.....	QVTL	
A1AA_RAT	..SDSE.....	QVTL	
O54913	..SDSE.....	QVTL	
A1AA_BOVIN	..SDSE.....	QVTL	
A1AA_CANFA	..SDSE.....	QVTL	
A1AA_RABIT	..SDSE.....	QVTL	
A1AA_HUMAN	..SDSE.....	QVTL	
A1AA_ORYLA	..SDSE.....	QVIL	
O96716	..SRNAFQGVVYSANQCKALITILVVLGAFMVTWG	PYMY	
O75963	..SLKAK	EGSTGTSESSVEARGSEEVRESSTVASDGSMEGKE	
HGPRBMY8			

FIG. 6F

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RYNPTSKWSKIKIVTKQTGTESVTAIEIVPAKAGASDHNS
YMKPEAKISKSVPIEKESAIQKREAKPMRSMVEISYEYKVY
.VHVRVGNKSKEHLPL...PSEAPT...PCAP...ASF
.VHVRVGNSKGDLPL...PSESCAT...SYVP...ACL
.VN...SNSKTHLPL...PN...T...P.QS...SSH
GYNSSSSSERLKQIQIETAEAFAN...GCAGEASTAML
RIHC...RGAT...GADGACHMRSAS
RIHC...RGAT...SAKGNPGTOSS
RIHR...KNAPA...CGGGVASA
RIHR...KNAPA...CGGGVASA
RIHR...KNAPA...CGGGVASA
RIHR...KNAPA...CGGGVASA
RIHR...KNVPA...EGSGVSSA
RIHR...KNQV...CGSGVTS
RIHR...KNAPV...CGHGVASA
RIHR...KNAPA...CGGGVASA
RIHR...KNPA...CGSGVASA
RIHR...GNTTV...SEDEAL
RLEQ...EN...NRGKKKSLA
VI...ASEALWGKSSVSPSLETWAT...WLSFASVCHPI
GSTVEENSMKADKGRTEVNCOSIDLGEDMEFEDDIN

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LNSRSPANVARKFAS...ARSQVRKKKQMAAR...EKKVTSST
 RHKNRKEIYRK...ROR...PKAISAAG...ERKGVVL
 ERK..NE...AEAKRKMA..LAR..ERKTVKTI
 ERK..NE...AEAKRKMA..LAR..ERKTVKTI
 ENI..NEKT...TGTRKMA..LAR..ERKTVKTI
 EQRCNNGKISSND...PYSRTRE...LKR..EKKAAPT
 KG...HTFRSSLSV...RLKK...FSR...EKKAAKTL
 KG...HTLRSSLSV...RLKK...FSR...EKKAAKTL
 KT...KT...HFSV...RLKK...FSR...EKKAAKTL
 KT...KT...HFSV...RLKK...FSR...EKKAAKTL
 KT...KT...HFSV...RLKK...FSR...EKKAAKTL
 KN...KT...HFSV...RLKK...FSR...EKKAAKTL
 KN...KT...HFSV...RLKK...FSR...EKKAAKTL
 KN...KT...HFSV...RLKK...FSR...EKKAAKTL
 KN...KT...HFSV...RLKK...FSR...EKKAAKTL
 KN...KT...HFSV...RLKK...FSR...EKKAAKTL
 KN...KT...HFSV...RLKK...FSR...EKKAAKTL
 KS...KT...HFA...RLKK...FSR...EKKAAKTL
 K...HFA...RLKK...FSR...EKKAAKTL
 LIYGLWNKTVRKELLMGCFGR...RYRPEFVQ...RORTSLF
 SEDDEAVNIPESLPPSRNSNS...NPPLPCYCOCAAKV

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FIG. 6G

ACM4_CHICK FATLLAFHLITPTNNVNLINFC..ETCVFET.VWS.GY
YDBM_CAEL GIDLGCTTCWAPFFIMYVLVQFC..KDCSPNAHTEMFTT
5H1A_HUMAN GIDMGTFILCWLPPFIFVALVLPF.CESSCHMPILLGAIIN
5H1A_MOUSE GIDMGTFILCWLPPFIFVALVLPF.CESSCHMPILLGAIIN
5H1A_FUGRU GIDMGTFILCWLPPFIFVALVLPF.CAENCYMPFWLGAMIN
5HT_LYMST IITIGAFILCWLPPFIFVALVLPF.VDFF.GIPPFARSEVL
A1AD_HUMAN GIVVGVFVLCWFPFFFVLPF.GSL.F.PQLKPSSEGVFKVIF
A1AD_MOUSE GIVVGVFVLCWFPFFFVLPF.GSL.F.PQLKPSSEGVFKVIF
Q13675 GIVVGVFVLCWLPFFFVLPF.PIGSF.F.PFKPSETVFKIIF
Q13729 GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF
060451 GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF
A1AA_RAT GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF
054913 GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF
A1AA_BOVIN GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF
A1AA_CANFA GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF
A1AA_RABIT GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF
A1AA_HUMAN GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF
A1AA_ORYLA GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF
096716 GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF
075963 GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF
HGPRBMY8 GIVVGVFVLCWLPFFVLPF.PIGSF.F.PFKPSETVFKIIF

ACM4_CHICK WLGYNSTINPACVLCNATFKKTEKHTLMCOYRNIGTAR
YDBM_CAEL WLGYSNSANPPIIYTVFNRLQINLKRIFTSEKKPSSSTR
5H1A_HUMAN WLGYSNSLNPPIIYAYFNKQONLKKKILCKCFQR~~~~
5H1A_MOUSE WLGYSNSLNPPIIYAYFNKQONLKKKILCKCFQR~~~~
5H1A_FUGRU WLGYSNSLNPPIIYAYFNKQONLKKKILCKCFHRH~~~~
5HT_LYMST WLGYNFNSLNPPIIYTIFFPEFNQFCKILFGKYRRGRH~~~
A1AD_HUMAN WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
A1AD_MOUSE WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
Q13675 WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
Q13729 WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
060451 WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
A1AA_RAT WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
054913 WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
A1AA_BOVIN WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
A1AA_CANFA WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
A1AA_RABIT WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
A1AA_HUMAN WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
A1AA_ORYLA WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
096716 WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
075963 WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.
HGPRBMY8 WLGYNFNSCNPPIIYPCSSQEFKKAFONVLR.LC.QCRRRRR.

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FIG. 6H

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ACM4_CHICK ~~~~~
YDBM_CAEEL V~~~~~
5H1A_HUMAN ~~~~~
5H1A_MOUSE ~~~~~
5H1A_FUGRU ~~~~~
5HT_LYMST ~~~~~
A1AD_HUMAN .RRPLWRVY..GHHWRASTSGIRQDCAPSSSGDAPPGAPLA
A1AD_MOUSE .R..LW.....PSLRPPLASI..DRRPALRLCPQPAHRT
Q13675 SKH...ALG..YT.LHPPSQAMEGQHKDM.VRIPVGSRET
Q13729 SKH...ALG..YT.LHPPSQAMEGQHKDM.VRIPVGSRET
O60451 SKH...ALG..YT.LHPPSQAMEGQHKDM.VRIPVGSRET
A1AA_RAT SKH...ALG..YT.LHPPSQAMEGQHRDM.VRIPVGSGET
O54913 SKH...ALG..YT.LHPPSQAMEEQHRGM.VRIPVGSGET
A1AA_BOVIN SKH...TLG..YT.LHAPSHVIEGQHKDL.VRIPVGSGET
A1AA_CANFA ~~~~~
A1AA_RABIT SKH...ALG..YT.LHAPSQAMEGQHKDM.VRIPVGSGET
A1AA_HUMAN SKH...ALG..YT.LHPPSQAMEGQHKDM.VRIPVGSRET
A1AA_ORYLA AHHHHLSVG..QSQTQGHSLTISLDSKGAPCRLSPSSSSVA
O96716 PNHADLNYDPVAMRLKKRGENANGTVNGDANGKANWIEA
O75963 ~~~~~
HGPRBMY8 EDSHPDLPGTGGTEGKIVPSYDSATFP~~~~~

ACM4_CHICK ~~~~~
YDBM_CAEEL ~~~~~
5H1A_HUMAN ~~~~~
5H1A_MOUSE ~~~~~
5H1A_FUGRU ~~~~~
5HT_LYMST ~~~~~
A1AD_HUMAN LTALPDPD..PEP...PGTPEMQAPVASRRKPESA...FR
A1AD_MOUSE PRGSPSPH..CTPR..PGLRRHAGGAGFGLRPSKASRLRLR
Q13675 FYRISKTDGVCWEKFFSSMPRGSARITVSKDQSSCTTART
Q13729 FYRISKTDGVCWEKFFSSMPRGSARITVSKDQSSCTTARG
O60451 FYRISKTDGVCWEKFFSSMPRGSARITVSKDQSSCTTARR
A1AA_RAT FYKISKTDGVCWEKFFSSMPQGSARITVPKQDSACTTARV
O54913 FYKISKTDGVCWEKFFSSMPQGSARITMPKQDSACTTARV
A1AA_BOVIN FYKISKTDGVCWEKIFSSSLPRGSARMMAVARDPSACTTARV
A1AA_CANFA ~~~~~
A1AA_RABIT FYKISKTDGVCWEKFFSSMPRGSARITVPKQDSACTTARV
A1AA_HUMAN FYRISKTDGVCWEKFFSSMPRGSARITVSKDQSSCTTARV
A1AA_ORYLA LSRT PSSRDSREWRVFSGGPINS..PGPTEAGRAKVAKL
O96716 GEGTSSS~
O75963 ~~~~~
HGPRBMY8 ~~~~~
```

D0047 NP

FIG. 6I

```
ACM4_CHICK ~~~~~
YDBM_CAEL ~~~~~
5H1A_HUMAN ~~~~~
5H1A_MOUSE ~~~~~
5H1A_FUGRU ~~~~~
5HT_LYMST ~~~~~
A1AD_HUMAN EWRLLGPFRRPTTQLRAKVSSLSHKIRAGGAQRAEAACAO
A1AD_MOUSE EWRLLGPLQRPTTQLRAKVSSLSHKFRSGGARRAETACAL
Q13675 KRSVTRLECS...GMILAHCN..LRLPGSRDSPASASQ
Q13729 HT.PMT~~~~~
O60451 GMDCRYFTKNC...REHIKHVN..FMMPWPWRKGLEC~~~~~
A1AA_RAT RSKSFLQVCCCV.GSSAPRPEEN..HQVPTIKIHTISLGE
O54913 RSKSFLQVCCCV.GSSTPRPEEN..HQVPTIKIHTISLGE
A1AA_BOVIN RSKSFLQVCCCL.GPSTPSHGEN..HQIPTIKIHTISLSE
A1AA_CANFA ~~~~~
A1AA_RABIT RSKSFLQVCCCV.GPSTPNNGEN..HQVPTIKIHTISLSE
A1AA_HUMAN RSKSFLQVCCCV.GPSTPSLDKN..HQVPTIKIHTISLSE
A1AA_ORYLA CNKSLHRTCCCILRARTPTQDPAPLGDLPTIKIHQLSLSE
O96716 ~~~~~
O75963 ~~~~~
HGPRBMY8 ~~~~~

ACM4_CHICK ~~~~~
YDBM_CAEL ~~~~~
5H1A_HUMAN ~~~~~
5H1A_MOUSE ~~~~~
5H1A_FUGRU ~~~~~
5HT_LYMST ~~~~~
A1AD_HUMAN RSEVEAVSLGVPHEVAEGATCQAYELADYSNLRETDI~~~~~
A1AD_MOUSE RSEVEAVSLNVPQDGAEAVICQAYEPGDLNLRETDI~~~~~
Q13675 AAGTTGDVPPGRRHQALIFVFLVETGFFHHVQGDDLDLLT
Q13729 ~~~~~
O60451 ~~~~~
A1AA_RAT NGEEV~~~~~
O54913 NGEEV~~~~~
A1AA_BOVIN NGEEV~~~~~
A1AA_CANFA ~~~~~
A1AA_RABIT NGEEV~~~~~
A1AA_HUMAN NGEEV~~~~~
A1AA_ORYLA KGESV~~~~~
O96716 ~~~~~
O75963 ~~~~~
HGPRBMY8 ~~~~~
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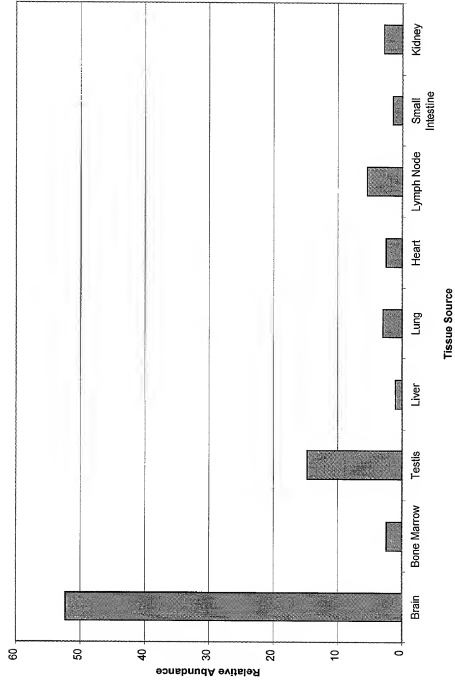
D0047 NP

FIG. 6J

ACM4_CHICK	~
YDBM_CAEEL	~
5H1A_HUMAN	~
5H1A_MOUSE	~
5H1A_FUGRU	~
5HT_LYMST	~
A1AD_HUMAN	~
A1AD_MOUSE	~
Q13675	S
Q13729	~
O60451	~
A1AA_RAT	~
O54913	~
A1AA_BOVIN	~
A1AA_CANFA	~
A1AA_RABIT	~
A1AA_HUMAN	~
A1AA_ORYLA	~
O96716	~
O75963	~
HGPREMY8	~

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FIG. 7



D0047 NP

FIG. 8

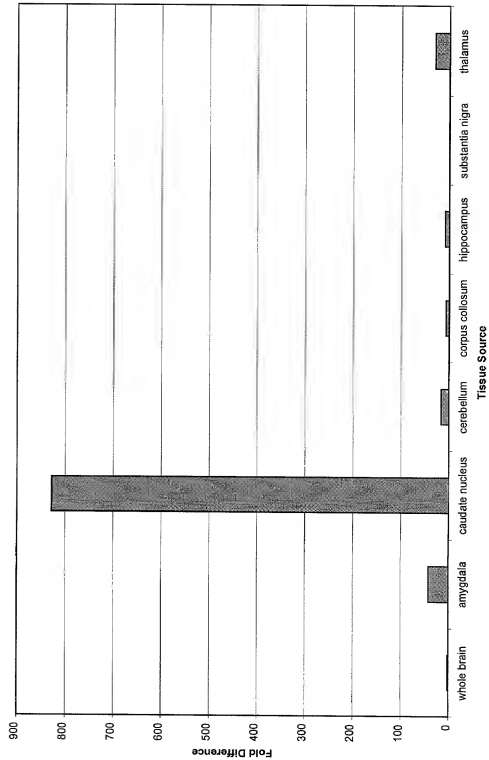


FIG. 9

HGPRBM8 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKF
 AL390879 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKF
 AX148250 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKF
 AX080495 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKF

HGPRBM8 QLLQVTNRFIFNLLVTDLLQISLVAPWVWVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
 AL390879 QLLQVTNRFIFNLLVTDLLQISLVAPWVWVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
 AX148250 QLLQVTNRFIFNLLVTDLLQISLVAPWVWVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
 AX080495 QLLQVTNRFIFNLLVTDLLQISLVAPWVWVATSVPLFWPLNSHFCTALVSLTHLFAFASVN

HGPRBM8 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
 AL390879 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
 AX148250 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
 AX080495 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA

HGPRBM8 LCSMIWGASPSYITILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
 AL390879 LCSMIWGASPSYITILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
 AX148250 LCSMIWGASPSYITILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
 AX080495 LCSMIWGASPSYITILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD

HGPRBM8 CVENEDEEGAEEKKEEFQDESEFRROHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
 AL390879 CVENEDEEGAEEKKEEFQDESEFRROHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
 AX148250 CVENEDEEGAEEKKEEFQDESEFRROHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA
 AX080495 CVENEDEEGAEEKKEEFQDESEFRROHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA

HGPRBM8 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMFEGEDDI
 AL390879 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMFEGEDDI
 AX148250 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMFEGEDDI
 AX080495 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMFEGEDDI

HGPRBM8 NFSEDDVEAVNIPESLPPSRNNSNPNPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV
 AL390879 NFSEDDVEAVNIPESLPPSRNNSNPNPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV
 AX148250 NFSEDDVEAVNIPESLPPSRNNSNPNPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV
 AX080495 NFSEDDVEAVNIPESLPPSRNNSNPNPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV

HGPRBM8 LAVVVDVETQVPQWVITIIIWLFLLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKP
 AL390879 LAVVVDVETQVPQWVITIIIWLFLLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKP
 AX148250 LAVVVDVETQVPQWVITIIIWLFLLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKP
 AX080495 LAVVVDVETQVPQWVITIIIWLFLLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKP

HGPRBM8 EDSDHPDLPGTEGGTEGKIVPSYDSATFF
 AL390879 EDSDHPDLPGTEGGTEGKIVPSYDSATFF
 AX148250 EDSDHPDLPGTEGGTEGKIVPSYDSATFF
 AX080495 EDSDHPDLPGTEGGTEGKIVPSYDSATFF

FIG. 10A

AX080495 GCCTGCAACCTGTCTCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGCG
 HGPRBM8 ~~~~GCAACCTGTCTCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGCG
 AL390879 ~~~~~~ATGACGTCCACCTGCG
 AX148250 ~~~~~~TGACGTCCACCTGCG

AX080495 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCTCTC
 HGPRBM8 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCTCTC
 AL390879 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCTCTC
 AX148250 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCTCTC

AX080495 CAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
 HGPRBM8 CAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
 AL390879 CAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG
 AX148250 CAAATGCCCATCAGCCTGGCCACGGCATCATCCGCTCAACCGTGCTGG

AX080495 TTATCTTCCTCGCCGCTCTTTTCGTGCGGAACATAGTGCTGGCGTAGTG
 HGPRBM8 TTATCTTCCTCGCCGCTCTTTTCGTGCGGAACATAGTGCTGGCGTAGTG
 AL390879 TTATCTTCCTCGCCGCTCTTTTCGTGCGGAACATAGTGCTGGCGTAGTG
 AX148250 TTATCTTCCTCGCCGCTCTTTTCGTGCGGAACATAGTGCTGGCGTAGTG

AX080495 TTGCAGCGCAAGCCGCGAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
 HGPRBM8 TTGCAGCGCAAGCCGCGAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
 AL390879 TTGCAGCGCAAGCCGCGAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
 AX148250 TTGCAGCGCAAGCCGCGAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA

AX080495 CCTCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCGCTGGGTGG
 HGPRBM8 CCTCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCGCTGGGTGG
 AL390879 CCTCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCGCTGGGTGG
 AX148250 CCTCTCGTCACCGACCTGCTGCAGATTTTCGCTCGTGGCCCGCTGGGTGG

AX080495 TGGCCACCTCTGTGCCTCTCTTTCTGGCCCTCAACAGCCACTTCTGCACG
 HGPRBM8 TGGCCACCTCTGTGCCTCTCTTTCTGGCCCTCAACAGCCACTTCTGCACG
 AL390879 TGGCCACCTCTGTGCCTCTCTTTCTGGCCCTCAACAGCCACTTCTGCACG
 AX148250 TGGCCACCTCTGTGCCTCTCTTTCTGGCCCTCAACAGCCACTTCTGCACG

AX080495 GCCCTGGTTAGCCTCACCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
 HGPRBM8 GCCCTGGTTAGCCTCACCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
 AL390879 GCCCTGGTTAGCCTCACCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT
 AX148250 GCCCTGGTTAGCCTCACCACCTGTTTCGCCTTCGCCAGCGTCAACACCAT

AX080495 TGTCTTGGTGTCACTGGATCGCTACTTGTCATCATCCACCTCTCTCTCT
 HGPRBM8 TGTCTTGGTGTCACTGGATCGCTACTTGTCATCATCCACCTCTCTCTCT
 AL390879 TGTCTTGGTGTCACTGGATCGCTACTTGTCATCATCCACCTCTCTCTCT
 AX148250 TGTCTTGGTGTCACTGGATCGCTACTTGTCATCATCCACCTCTCTCTCT

AX080495 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC
 HGPRBM8 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC
 AL390879 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC
 AX148250 ACCCGTCCAAGATGACCCAGCGCCGCGTTACCTGCTCCTCTATGGCACC

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FIG. 10B

AX080495 TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
HGPRBM8 TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AL390879 TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX148250 TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA

AX080495 GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
HGPRBM8 GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AL390879 GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX148250 GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA

AX080495 GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
HGPRBM8 GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AL390879 GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG
AX148250 GCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCATCGTCATTCCACTG

AX080495 ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCCGAGGCA
HGPRBM8 ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCCGAGGCA
AL390879 ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCCGAGGCA
AX148250 ATTGTCATGATTGCCTGCTACTCCGTGGTGTCTGTGCAGCCCCGAGGCA

AX080495 GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
HGPRBM8 GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
AL390879 GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA
AX148250 GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGAAGTGCGAGTCA

AX080495 AGGACTGTGTGGAGAAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
HGPRBM8 AGGACTGTGTGGAGAAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AL390879 AGGACTGTGTGGAGAAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX148250 AGGACTGTGTGGAGAAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG

AX080495 TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
HGPRBM8 TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AL390879 TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX148250 TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC

AX080495 CAAGGAGGGCAGAAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
HGPRBM8 CAAGGAGGGCAGAAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AL390879 CAAGGAGGGCAGAAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX148250 CAAGGAGGGCAGAAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG

AX080495 GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
HGPRBM8 GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AL390879 GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX148250 GAAGCACGGGGACCACTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG

AX080495 GTCAGAGAGAGCAGCACGGTGGCCAGCGCAGCGCAGCATGGAGGGTAAGGA
HGPRBM8 GTCAGAGAGAGCAGCACGGTGGCCAGCGCAGCGCAGCATGGAGGGTAAGGA
AL390879 GTCAGAGAGAGCAGCACGGTGGCCAGCGCAGCGCAGCATGGAGGGTAAGGA
AX148250 GTCAGAGAGAGCAGCACGGTGGCCAGCGCAGCGCAGCATGGAGGGTAAGGA

FIG. 10B

AX080495 TGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCT
 HGPRBM8 TGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCT
 AL390879 TGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCT
 AX148250 TGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCT

AX080495 CAGAGGTCAACCCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
 HGPRBM8 CAGAGGTCAACCCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
 AL390879 CAGAGGTCAACCCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
 AX148250 CAGAGGTCAACCCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT

AX080495 GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
 HGPRBM8 GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
 AL390879 GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
 AX148250 GGTGAAGACGACATCAATTTTCAGTGAGGATGACGTCGAGGCAGTGAACAT

AX080495 CCCGGAGAGCCTCCCACCCAGTCGTCGTAAACAGCAACAGCAACCCTCCTC
 HGPRBM8 CCCGGAGAGCCTCCCACCCAGTCGTCGTAAACAGCAACAGCAACCCTCCTC
 AL390879 CCCGGAGAGCCTCCCACCCAGTCGTCGTAAACAGCAACAGCAACCCTCCTC
 AX148250 CCCGGAGAGCCTCCCACCCAGTCGTCGTAAACAGCAACAGCAACCCTCCTC

AX080495 TGCCCAGGTGCTACCCAGTGCAAAGCTGCTAAAGTGATCTTCATCATCATT
 HGPRBM8 TGCCCAGGTGCTACCCAGTGCAAAGCTGCTAAAGTGATCTTCATCATCATT
 AL390879 TGCCCAGGTGCTACCCAGTGCAAAGCTGCTAAAGTGATCTTCATCATCATT
 AX148250 TGCCCAGGTGCTACCCAGTGCAAAGCTGCTAAAGTGATCTTCATCATCATT

AX080495 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTATAGCAGTCCTGGC
 HGPRBM8 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTATAGCAGTCCTGGC
 AL390879 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTATAGCAGTCCTGGC
 AX148250 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTATAGCAGTCCTGGC

AX080495 CGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATTAA
 HGPRBM8 CGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATTAA
 AL390879 CGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATTAA
 AX148250 CGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATTAA

AX080495 TCATCTGGCTTTTCTTCCTGCAGTGTGCATCCACCCCTATGTCTATGGC
 HGPRBM8 TCATCTGGCTTTTCTTCCTGCAGTGTGCATCCACCCCTATGTCTATGGC
 AL390879 TCATCTGGCTTTTCTTCCTGCAGTGTGCATCCACCCCTATGTCTATGGC
 AX148250 TCATCTGGCTTTTCTTCCTGCAGTGTGCATCCACCCCTATGTCTATGGC

AX080495 TACATGCACAAGACCATTAAAGAGGAAATCCAGGACATGCTGAAGAAGTT
 HGPRBM8 TACATGCACAAGACCATTAAAGAGGAAATCCAGGACATGCTGAAGAAGTT
 AL390879 TACATGCACAAGACCATTAAAGAGGAAATCCAGGACATGCTGAAGAAGTT
 AX148250 TACATGCACAAGACCATTAAAGAGGAAATCCAGGACATGCTGAAGAAGTT

AX080495 CTTCTGCAAGGAAAAGCCCCCGAAAAGATAGCCACCCAGACCTGCCCG
 HGPRBM8 CTTCTGCAAGGAAAAGCCCCCGAAAAGATAGCCACCCAGACCTGCCCG
 AL390879 CTTCTGCAAGGAAAAGCCCCCGAAAAGATAGCCACCCAGACCTGCCCG
 AX148250 CTTCTGCAAGGAAAAGCCCCCGAAAAGATAGCCACCCAGACCTGCCCG

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FIG. 10D

AX080495	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCTTCCTACGATTCTGCT
HGPRBMY8	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCTTCCTACGATTCTGCT
AL390879	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCTTCCTACGATTCTGCT
AX148250	GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCTTCCTACGATTCTGCT
AX080495	ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTTGAAAAATCAGTCCTTCA
HGPRBMY8	ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTT~~~~~
AL390879	ACTTTTCCTTG/~~~~~
AX148250	ACTTTTCCTTG/~~~~~
AX080495	GCCACAGCTATTTAGAGCTTTAAAACTACCAGGTTCAATCACTGGTTATG
HGPRBMY8	~~~~~
AL390879	~~~~~
AX148250	~~~~~
AX080495	CTTTCTGTG
HGPRBMY8	~~~~~
AL390879	~~~~~
AX148250	~~~~~

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FIG. 11

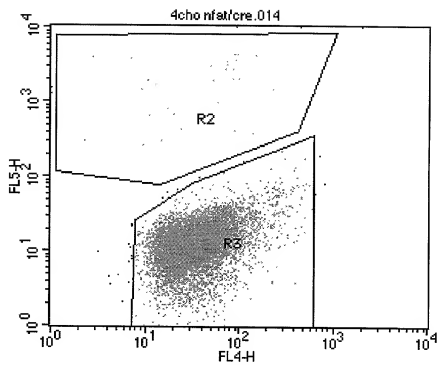


FIG. 12

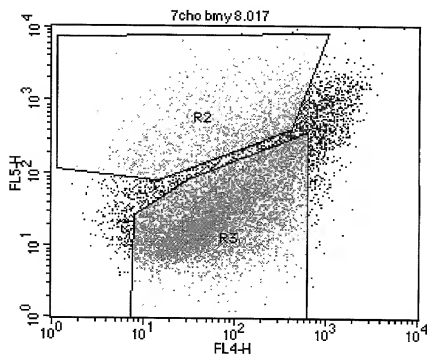


FIG. 13

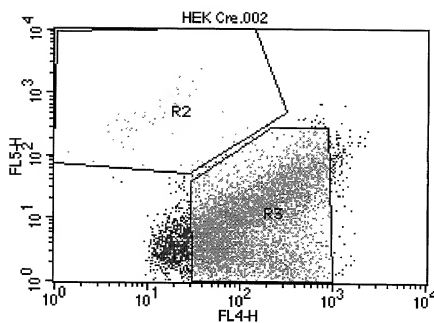


FIG. 14

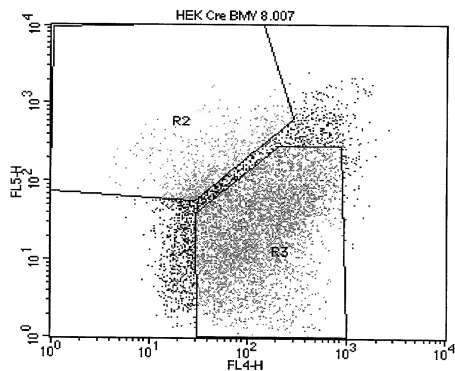
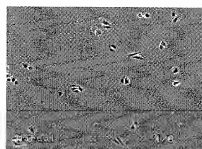


FIG. 15

a. CHO-NFAT G alpha 15 (Fluorescent vs. Bright Field)



b. CHO-NFAT/ G alpha 15 HGPRBMY8 (Fluorescent vs. Bright Field)

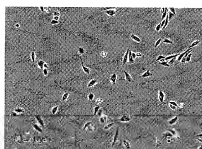
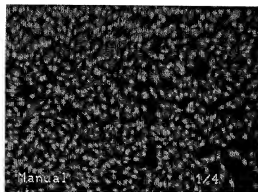


FIG. 16

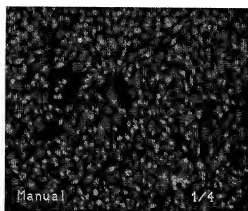
a. CHO-NFAT/CRE



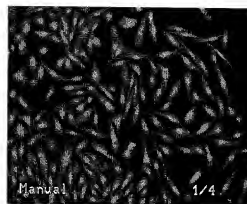
b. CHO-NFAT/CRE + F/T/P



c. CHO-NFAT/CRE oGPCR-Intermediate



d. CHO-NFAT/CRE oGPCR high



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FIG. 17

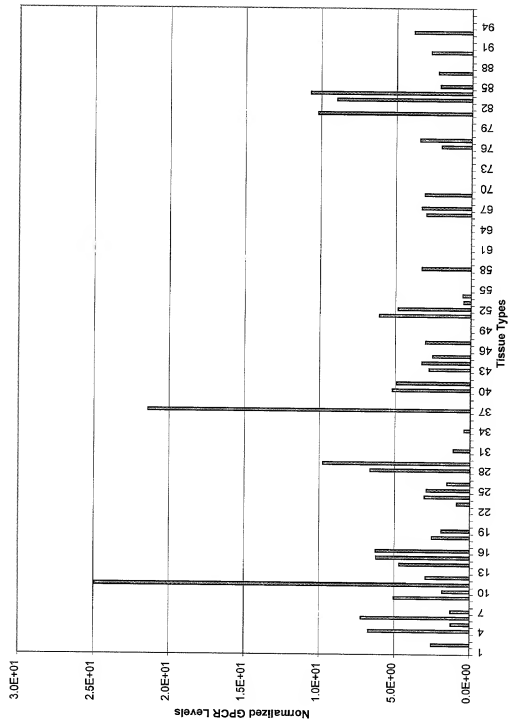


FIG. 18A

1	ATGAGCTGTCACCTGCACCAACAGCAAGCGGGAGAGTAAACAGCAGCCACAGTGCATGCC	1
1	M T S T C T C T N S T R E S N S S H T C M P	20
61	CTCTCAAAATGCCCATCAGCCTGGGCCACGGCATCATCGCTCAACCGTGTGGTTATC	120
21	L S K M P I S L A H G I I R S T V L V I	40
121	TTCTCGCGCGCTCTTTCTGGCGCAACATAGTCTGGCGCTAGTGTTCAGCGCAAGCGG	180
41	F L A A S F V G N I V L A L V L Q R K P	60
181	CAGCTGCTGCAGGTGACCAACCGTTTATCTTTAACTCTCTGTCACCGACTGCTGCAG	240
61	Q L L Q V T N R F I F N L L V T D L L Q	80
241	ATTTCTGCTGTTGGGCCCCCTGGTGGTGGCCACCTCTGTGCCTCTCTTCTGGCCCCCAAC	300
81	I S L V A P W V V A T S V P L F W F L N	100
301	AGCCACTTCTGCAGCGCCCTGGTGTAGCCTCACCCACCTGTTCGCTTCCGCCAGCGCTCAAC	360
101	S H F C T A L V S L T H L F A F A S V N	120
361	ACCATTGTCTTGGTGTGAGTGATCGTACTTGTCCATCATCCACCTCTCTCTTACC	420
121	T I V X V S V D R Y L S I I H P L S Y P	140
421	TCCAAGATGACCCAGCGCCCGGTGTACCTGTCTCTATGGCACCTGGATTGTGCCATC	480
141	S K M T Q R R G Y L L L Y G T W I V A I	160
481	CTGCAGAGCACTCTCTCACTTACGGGTGGGGCCAGGCTGCCTTGTATGAGCGCAATGCT	540
161	L Q S T P P L Y G W G Q A A F D E R N A	180
541	CTCTGCTCCATGATCTGGGGGGCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCTTCT	600
181	L C S M I W G A S P S Y T I L S V V S F	200
601	ATCGTCATTCCAATGATTGTATGATGTGCTGCTACTCGTGGTGTCTCTGTGCAGCCCGG	660
201	I V I P L I V M I A C Y S V V F C A A R	220
661	AGGCAGCATGCTCTGCTGTACATGTCAAGAGACACAGCTTGGAGTGCGAGTCAAGGAC	720
221	R Q H A L L Y N V K R H S L E V R V K D	240
721	TGTGTGGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTTCACGATGAGAGT	780
241	C V E N E D E E G A E K K E E F Q D E S	260
781	GAGTTTCGCGCCAGCATGAGGTGAGGTCAAGGCCAAGGAGGGCAGATGGAAGCCAAG	840
261	E F R R Q H E G E V K A K E G R M E A K	280
841	GACGGCAGCCTGACCAAGGAAGGAACCGGGGACAGTGAGATAGTGTAGAGGCC	900
281	D G S L K A K E G S T G T S E S S V E A	300

FIG. 18B

901 AGGGGCAGCGAGGAGGTGAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT 960
 301 R G S E E V R E S S T V A S D G S M E G 320

961 AAGGAAGGCAGCACCAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCACAGAG 1020
 321 K E G S T K V E E N S M K A D K G R T E 340

1021 GTCAACCAGTGCAGCATTGACTTGGGTGAAGATGNCATGGAGTTTGGTGAAGACGACATC 1080
 341 V N Q C S I D L G E D X M E F G E D D I 360

1081 AATTTTCAGTGAGGATGACGTCGAGGCGAGTGAACATCCCGGAGAGCCTCCCACCCAGTCGT 1140
 361 N F S E D D V E A V N I P E S L P P S R 380

1141 CGTAACAGCAACAGCAACCCCTCTGCCCAGGTGCTACCACTGCAAGCTNNNAAGTG 1200
 381 R N S N S N P P L P R C Y Q C K A X K V 400

1201 ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTCAGAGTC 1260
 401 I F I I I F S Y V L S L G P Y C F L A V 420

1261 CTGGCCGTGTGGGTGGATGTCGAAACCCAGGTACCCAGTGGGTGATCACCATAATCATC 1320
 421 L A V W V D V E T Q V P Q W V I T I I I 440

1321 TGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGCTACATGCACCAAGCC 1380
 441 W L F F L Q C C I H P Y V Y G Y M H K T 460

1381 ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTCTGCAAGGAAAGCCCCGGAAA 1440
 461 I K K E I Q D M L K K F F C K E K P P K 480

1441 GAAGATAGCCACCCAGACCTGCCCGAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT 1500
 481 E D S H P D L P G T E G G T E G K I V P 500

1501 TCCTACGATTCTGCTACTTTTCCTTGA 1527
 501 S Y D S A T F P 508